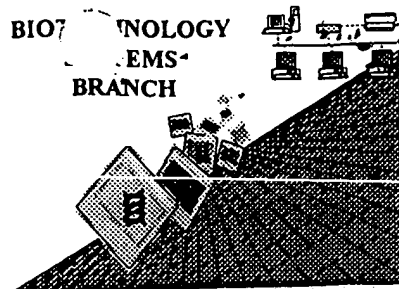


BEST AVAILABLE COPY

BIO7 TECHNOLOGY
EMS-
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/787986

Source: PCT09

Date Processed by STIC: 9/13/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/787986

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,986

DATE: 09/13/2001

TIME: 17:28:24

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\09132001\I787986.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Lewis, Richard J.
 5 Alewood, Paul F.
 6 Sharpe, Iain A.
 8 <120> TITLE OF INVENTION: NOVEL PEPTIDES
 10 <130> FILE REFERENCE: Davies Collison Cave
 12 <140> CURRENT APPLICATION NUMBER: 09/787,986
 13 <141> CURRENT FILING DATE: 1999-10-01
 15 <160> NUMBER OF SEQ ID NOS: 9
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 13
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Conus marmoreus
 24 <220> FEATURE:
 25 <221> NAME/KEY: PEPTIDE
 26 <222> LOCATION: (12)
 27 <223> OTHER INFORMATION: Xaa at position 12 is 4Hyp.
 29 <400> SEQUENCE: 1
 W--> 30 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys
 31 1 5 10
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 13
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Conus marmoreus
 39 <220> FEATURE:
 40 <221> NAME/KEY: PEPTIDE
 41 <222> LOCATION: (12)
 42 <223> OTHER INFORMATION: Xaa at position 12 is 4Hyp
 44 <400> SEQUENCE: 2
 W--> 45 Val Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys
 46 1 5 10
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 13
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Conus marmoreus
 54 <400> SEQUENCE: 3
 55 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys
 56 1 5 10
 59 <210> SEQ ID NO: 4
 60 <211> LENGTH: 20
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Artificial Sequence
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: Description of Artificial Sequence:
 66 Oligonucleotide probe
 68 <400> SEQUENCE: 4
 W--> 69 canggrtgrc anarytttrta

*Errors Sequence**Unknown nucleotide bases
must be described in field**221 as unsure, 222 at
specific location, and
223 by possible base values.*

RAW SEQUENCE LISTING

DATE: 09/13/2001

PATENT APPLICATION: US/09/787,986

TIME: 17:28:24

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\09132001\I787986.raw

```

73 <210> SEQ ID NO: 5
74 <211> LENGTH: 27
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence:
80     Oligonucleotide probe
82 <400> SEQUENCE: 5
83 ccatacctaatac gactcact atagggc                27
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 23
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:
94     Oligonucleotide probe
96 <400> SEQUENCE: 6
97 acaggcagaa tgcgctgtct ccc                23
101 <210> SEQ ID NO: 7
102 <211> LENGTH: 28
103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Description of Artificial Sequence:
108     Oligonucleotide probe
110 <400> SEQUENCE: 7
111 aactggaaga attcgcggcc gcaggaat                28
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 186
117 <212> TYPE: DNA
118 <213> ORGANISM: Conus marmoreus
120 <400> SEQUENCE: 8
121 atgcgctgtc tcccagtctt gatcattctt ctgctgctga ctgcatctgc acctggcggt 60
123 gttgtcctac cgaagaccga agatgatgtg cccatgtcat ctgtctactg taatggaaag 120
125 agtatacctac gaggaattct gaggaacggt gtgtgctgtg gctataagtt gtgccatcca 180
127 tgtaa                186
131 <210> SEQ ID NO: 9
132 <211> LENGTH: 61
133 <212> TYPE: PRT
134 <213> ORGANISM: Conus marmoreus
136 <400> SEQUENCE: 9
137 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
138   1           5           10           15
140 Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met
141           20           25           30
143 Ser Ser Val Tyr Cys Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg
144           35           40           45
146 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys
147           50           55           60

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/767,936

DATE: 09/13/2001

TIME: 17:28:26

Input Set : A:\SEQUENCE.asc

Output Set: N:\CRF3\09132001\I787986.raw

L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4